

Db 452 GCAACTACATGATCGGGTGGCCACACCCAGGCCATCCGGGACGCCAGGGTCTACTGG 511
 QY 483 CTTGGGATGAGCTAGAGGAGCCCTGAGGCTCAACTATGTGCTCAAGAGACACCGGGATG 542
 Db 512 CTTGGGATGAGCTAGAGGAGCCCTGAGGCTCAACTATGTGCTCAAGAGACACCGGGATG 571
 QY 543 TGCAGCTACACTCTCTCCAGGCAACAGCTCTACCACTCATCGAATTTGGCCACT 602
 Db 572 TGCAGCTACACTCTCTCCAGGCAACAGCTCTACCACTCATCGAATTTGGCCACT 631
 QY 603 ACCGCTCCCTGAGGAGCCCTGCTGATCCGCAACCCATTCCTCCCTCCATGGCCAAAA 662
 Db 632 ACCGCTCCCTGAGGAGCCCTGCTGATCCGCAACCCATTCCTCCCTCCATGGCCAAAA 691
 QY 663 CCCCACTGTCTCTCTCCCAATAAAGATGAGTCTC 697
 Db 692 CCCCACTGTCTCTCTCCCAATAAAGATGAGTCTC 726

RESULT 6
 AR226480 749 bp DNA linear PAT 20-DEC-2002
 LOCUS Sequence 5 from patent US 6444799
 DEFINITION AR226480
 ACCESSION AR226480.1 GI:27265028
 VERSION
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.

REFERENCE 1 (bases 1 to 749)
 AUTHORS Young, P.E., Ruben, S.M., Rosen, C.A. and Olsen, H.S.
 TITLE Peptidoglycan recognition proteins
 JOURNAL Patent: US 6444790-A 5 03-SEP-2002;
 FEATURES Location/Qualifiers
 source 1..749
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN

Query Match 99.7%; Score 695; DB 6; Length 749;
 Best Local Similarity 100.0%; Pred. No. 3,2e-143;
 Matches 695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCGGACCCCTGCGCCCTTGCCTATATGCTGCTTGCCTGAGGCTCTCC 62
 Db 32 CCGGACCCCTGCGCCCTTGCCTATATGCTGCTTGCCTGAGGCTCTCC 91
 QY 63 CCGGACCCCTGCGCCCTTGCCTATATGCTGCTTGCCTGAGGCTCTCC 122
 Db 92 CCGGACCCCTGCGCCCTTGCCTATATGCTGCTTGCCTGAGGCTCTCC 151
 QY 123 TAGTGGCCCGGAAAGAGTGAAGGCGCTGCAATGAGTGGCCCGCACTGAGCTGAC 182
 Db 152 TAGTGGCCCGGAAAGAGTGAAGGCGCTGCAATGAGTGGCCCGCACTGAGCTGAC 211
 QY 183 CCTTAGGCTATGAGTGGTATGAGCAACGCGGCGGAGGCTGCAACCCCGCTTGT 242
 Db 212 CCTTAGGCTATGAGTGGTATGAGCAACGCGGCGGAGGCTGCAACCCCGCTTGT 271
 QY 243 GCCAGAGCAGGCGCCGGAATGTGACAGCACTACCAATGAAGCACTGGGGCTGGAGAG 302
 Db 272 GCCAGAGCAGGCGCCGGAATGTGACAGCACTACCAATGAAGCACTGGGGCTGGAGAG 331
 QY 303 TGGGCTACAACTTCTGATTTGGAAGACGGGCTGATATGAGGCGCGTGGTGAAC 362
 Db 332 TGGGCTACAACTTCTGATTTGGAAGACGGGCTGATATGAGGCGCGTGGTGAAC 391
 QY 363 TCAAGGAGTGGCCACTGAGTCACTTATGAGACCCCAATGCAATGGCAATGAGCTTCAAG 422
 Db 392 TCAAGGAGTGGCCACTGAGTCACTTATGAGACCCCAATGCAATGGCAATGAGCTTCAAG 451

Db 452 GCAACTACATGATCGGGTGGCCACACCCAGGCCATCCGGGACGCCAGGGTCTACTGG 511
 QY 483 CTTGGGATGAGCTAGAGGAGCCCTGAGGCTCAACTATGTGCTCAAGAGACACCGGGATG 542
 Db 512 CTTGGGATGAGCTAGAGGAGCCCTGAGGCTCAACTATGTGCTCAAGAGACACCGGGATG 571
 QY 543 TGCAGCTACACTCTCTCCAGGCAACAGCTCTACCACTCATCGAATTTGGCCACT 602
 Db 572 TGCAGCTACACTCTCTCCAGGCAACAGCTCTACCACTCATCGAATTTGGCCACT 631
 QY 603 ACCGCTCCCTGAGGAGCCCTGCTGATCCGCAACCCATTCCTCCCTCCATGGCCAAAA 662
 Db 632 ACCGCTCCCTGAGGAGCCCTGCTGATCCGCAACCCATTCCTCCCTCCATGGCCAAAA 691
 QY 663 CCCCACTGTCTCTCTCCCAATAAAGATGAGTCTC 697
 Db 692 CCCCACTGTCTCTCTCCCAATAAAGATGAGTCTC 726

RESULT 7
 BD078857 718 bp DNA linear PAT 27-AUG-2002
 LOCUS Tumor proliferation inhibition- and apoptosis-associated gene and
 DEFINITION polypeptide and method of using the same.
 ACCESSION BD078857
 VERSION BD078857.1 GI:22624460
 KEYWORDS JP 2001509384-A/2.
 SOURCE JP 2001509384-A/2.
 ORGANISM Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 718)
 AUTHORS Georgiev, G., Kiselev, S., Prokhorchouk, E. and Ostermann, E.
 TITLE Tumor proliferation inhibition- and apoptosis-associated gene and
 JOURNAL polypeptide and method of using the same
 Patent: JP 2001509384-A 2 24-JUL-2001;
 BOEHRINGER INGELHEIM INTERNATIONAL GMBH
 OS Homo sapiens (human)
 PN UP 2001509384-A/2
 PD 24-JUL-2001
 PF 10-JUL-1998 JP 2000502182
 PR 11-JUL-1997 US 08/893764
 PI GEORGII GEORGIEV, SERGEI KISELEV, EGOR PROKHORCHOUK, ELINBOG PI
 OSTERMANN

COMMENT

PC C12N15/09, A61K35/76, A61K38/00, A61K48/00, A61P35/00, C07K14/525,
 PC C07K16/24,
 PC C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/02, C12P21/08 PC
 C12O1/68, G01N33/53,
 PC C12N15/00, A61K37/02, C12N5/00
 CC Tumor proliferation inhibition- and apoptosis-associated gene
 CC and
 CC polypeptide and method of using the same
 FH key Location/Qualifiers
 FT 1..67
 FT CDS 68..643
 FT 3'UTR 644..718
 FT polyA site 712..718
 Location/Qualifiers
 1..718
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

ORIGIN

Query Match 96.7%; Score 674; DB 6; Length 718;
 Best Local Similarity 98.6%; Pred. No. 1.4e-138;
 Matches 680; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2 CCGGACCCCTGCGCCCTTGCCTATATGCTGCTTGCCTGAGGCTCTCC 61
 Db 29 CCGGACCCCTGCGCCCTTGCCTATATGCTGCTTGCCTGAGGCTCTCC 98

Mon May 17 11:03:28 2004

us-10-015-390a-216.rge

Page 1

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Comphen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 16, 2004, 15:44:42 ; Search time 3727 Seconds
(without alignments)
2279.376 Million cell updates/sec

Title: US-10-015-390A-216
Perfect score: 1074
Sequence: 1 MSRRSMILMALPDLRLGN.....LSRGNQYHLIQWPHYRSP 196

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+P2n.model -DEV=xlh
-O=/cgn1/USPRO/spool/US10015390/runcat_13052004_145023_2376/app_query.fasta_1.391
-DB=genmb1 -OPMT=fastap -SUFFIX=rgc -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTWT=ptio -NORM=ext -HEAPSIZE=570 -MINLEN=0 -MAXLEN=2000000000
-USER=US10015390@cgn 1.1 3508 @runcat_13052004_145023_2376 -NCPU=6 -ICPU=3
-NO MMAP -LARGEOUTRY -NEG_SCORES=0 -WAIT -DSRBLCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
GenEmbl:*
1: gb_ba:*
2: gb_bhg:*
3: gb_in:*
4: gb_in:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_to:*
11: gb_bys:*
12: gb_by:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_to:*
27: em_vl:*
28: em_un:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Match Length	DB ID	Description
1	1074	100.0	9 AF076483	AF076483 Homo sapi
2	1074	100.0	6 AX697147	AX697147 Sequence
3	1074	100.0	6 AY358936	AY358936 Homo sapi
4	1074	100.0	7 BD078857	BD078857 Tumor pro
5	1074	100.0	6 AF242517	AF242517 Homo sapi
6	1074	100.0	6 BD261706	BD261706 12 human
7	1074	100.0	6 BD267640	BD267640 Peptidogl
8	1074	100.0	6 AR226480	AR226480 Sequence
9	989	92.1	6 AX78312	AX78312 Sequence
10	782	72.8	700 4 CDR131676	CDR131676 Camelus d
11	730	68.0	688 4 AY083309	AY083309 Bos tauru
12	696	64.8	669 10 AF193843	AF193843 Mus muscu
13	686	64.8	680 10 AF075482	AF075482 Sequence
14	686	64.8	713 10 BC005582	BC005582 Mus muscu
15	692	64.4	549 6 AR124884	AR124884 Sequence
16	692	64.4	6 BD078856	BD078856 Tumor pro
17	673.5	62.7	630 10 AF154114	AF154114 Rattus no
18	654.5	60.9	678 10 MKNRATMS1	MKNRATMS1
19	596	55.5	380 6 BD204097	BD204097 5'EST and
20	523	48.7	166500 9 AC007785	AC007785 Homo sapi
21	441.5	41.1	1173 9 AF035376	AF035376 Homo sapi
22	417.5	38.9	555 3 DS155611	DS155611 Drosophi
23	415.5	38.7	555 3 DMS55614	DMS55614 Drosophi
24	415.5	38.7	555 3 DMS55615	DMS55615 Drosophi
25	415.5	38.7	555 3 DMS55616	DMS55616 Drosophi
26	415.5	38.7	555 3 DMS55617	DMS55617 Drosophi
27	415.5	38.7	555 3 DMS55618	DMS55618 Drosophi
28	415.5	38.7	555 3 DMS55620	DMS55620 Drosophi
29	415.5	38.7	555 3 DMS55621	DMS55621 Drosophi
30	414.5	38.6	555 3 DMS55612	DMS55612 Drosophi
31	414.5	38.6	555 3 DMS55613	DMS55613 Drosophi
32	414.5	38.6	555 3 DMS55619	DMS55619 Drosophi
33	414.5	38.6	555 3 DMS55622	DMS55622 Drosophi
34	414.5	38.6	166867 3 AC007085	AC007085 Drosophi
35	414.5	38.6	169509 3 AC007303	AC007303 Drosophi
36	414.5	38.6	172838 2 AC020451	AC020451 Drosophi
37	414.5	38.6	259383 3 AE003836	AE003836 Drosophi
38	413	38.5	1110 6 AX119918	AX119918 Sequence
39	413	38.5	1128 6 AX119915	AX119915 Sequence
40	405.5	37.8	558 3 DMS55658	DMS55658 Drosophi
41	405.5	37.8	558 3 DMS55659	DMS55659 Drosophi
42	405.5	37.8	558 3 DMS55658	DMS55658 Drosophi
43	405.5	37.8	558 3 DMS55659	DMS55659 Drosophi
44	405.5	37.8	558 3 DMS55659	DMS55659 Drosophi
45	405.5	37.8	558 3 DMS55659	DMS55659 Drosophi

RESULT 1

ALIGNMENTS

146 GCCCTGGCATCAGATGCGCCGACGACCTGAGCCTGCTTACGCTATGTGTGATG 205
QY HisThrAlaGlySerSerCysAsnThrProAlaSerCysGlnGlnGlnAlaArgAsnVal 80
Db CACACGGCGGGGACGAGCTGACACACCCCGCTCGTGGCCAGCAGCGCCGGAATGTG 265
QY GlnHisThrHisMetCysThrLeuGlyTTPCysAspValGlyTyrAsnPhenLeuIleGly 100
Db CAGACACTACCACTGAGACACTGGGCTGTGGCACTGGGCTTACCACTTCTGATTTGA 325
QY GlnAspGlyLeuValTyrGlnGlyTyrGlyTyrAsnPhenThrGlyAlaHisSerGlyHis 120
Db GAGACGGGCTCGTATGCGAGGGCGCTGCTGAACTTCAAGGCTGCCCTCAGGTAC 385
QY LeuTyrAsnProMetSerIleGlyIleSerPheMetGlyAsnTyrMetAspArgValPro 140
Db TTATGGAACCCCATGCTCATGTGGCATGCTTCACTGAGCACTACATGATGCGGTGCCC 445
QY 141 ThrProGlnAlaIleArgAlaAlaGlnGlyLeuLeuAlaCysGlyValAlaGlnGlyAla 160
Db 446 ACACCCCAAGCCGATCCGGGACGCGCAGGAGTCTACTGCGCTGCGGTGCTCAGGAGCC 505
QY 161 LeuArgSerAsnTyrValLeuTyrGlyHisArgAspValGlnArgThrLeuSerProGly 180
Db 506 CTGAGGTCCCACTATGTGCTCAAGAGACACCGGGATGTGACGATGACACTCTCTCCAGGC 565
QY 181 AsnGlnLeuTyrHisLeuIleGlnAsnTyrProHisTyrArgSerPro 196
Db 566 AACCACTCTACCACTCATCAGAAATGGCCACACTACCGCTCCCCC 613

RESULT 3
AY358936 697 bp mRNA linear PRI 03-OCT-2003
LOCUS Homo sapiens clone DNA6520 Granulocyte pep A (UNQ639) mRNA.
DEFINITION complete cds.
ACCESSION AY358936
VERSION AY358936.1 GI:37182989
KEYWORDS FLI CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 697)
AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Haas,P.E.,
Heidens,S., Huang,A., Kim,H.S., Klimoweki,L., Jin,Y., Johnson,S.,
Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,
Schonfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,
Stinson,U., Vagts,A., Vandlen,R., Watanabe,C., Weand,D., Woods,K.,
Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
Goddard,A., Wood,W.I. and Godowski,P.
The Secreted Protein Discovery Initiative (SPDI), a Large-scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins:
A Bioinformatics Assessment
Genome Res. 13 (10), 2265-2270 (2003)

JOURNAL PDBMED 12975309
PUBMED 2 (bases 1 to 697)
REFERENCE Clark,H.F.
AUTHORS Direct Submission
TITLE Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
JOURNAL Inc., 1 DNA Way, South San Francisco, CA 94080, USA
FEATURES
source location/Qualifiers
1..697
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DNA6520"
1..697
/locus_tag="UNQ639"
26..616
/locus_tag="UNQ639"
/note="PRO1269"

/codon_start=1
/product="Granulocyte pep A"
/protein_id="AA089295.1"
/db_xref="GI:37182989"
/translation="MSRRSMDLAALWALPSLRGAODETDPACSPVPRNEMTALAS
EAOHLISLPLRYVYSHYASGSCNTTPASCCOQAOAVQHYHMKTLGMDGVNPLIGED
GLVYEGRNFTGASHGIMWPMNSIGTISFMGNVMDRVPPTPAIRAAQGLAACGVAQGA
LRNRYVLKGRHMDVORTLSPGNQLPHLIQNMHRYSP"

ORIGIN
Alignment Scores:
Pred. No.: 3,686-93 Length: 697
Score: 1074.00 Matches: 196
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-10-015-390A-216 (1-196) x AY358936 (1-697)

QY 1 MetSerArgArgSerMetLeuLeuAlaThrAlaLeuProSerLeuLeuArgLeuGlyVala 20
Db 26 ATGTCCCGCGCTCTATGTGCTTGTCTGCGGCTCTCCAGGCTCTTCCAGCTCGAGACG 85
QY 21 AlaGlnGlnThrGlnAspProAlaCysCysSerProIleValProArgAsnGlnTrrlys 40
Db 86 GCTCAGAGACAGAAAGACCCGCGCTGTGACGCCCCCATATGTCGCCGAGACGATGGAAG 145
QY 41 AlaLeuAlaSerGlnCysAlaGlnHisLeuSerLeuProLeuArgTyrValValaSer 60
Db 146 GCCCTGGCATCAGATGCGCCGACGACCTGAGCCTGCGCTTACGCTATGTGTGATG 205
QY 61 HisThrAlaGlySerSerCysAsnThrProAlaSerCysGlnGlnGlnAlaArgAsnVal 80
Db 206 CACACGGCGGGGACGAGCTGACACACCCCGCTCGTGGCCAGCAGCGCCGGAATGTG 265
QY 81 GlnHisThrHisMetCysThrLeuGlyTTPCysAspValGlyTyrAsnPhenLeuIleGly 100
Db 266 CAGCACTACCACTATGTGCTCAAGAGACACCGGGATGTGACGATGACACTCTCTCCAGGC 325
QY 101 GlnAspGlyLeuValTyrGlnGlyTyrArgGlyTTPAsnPhenThrGlyAlaHisSerGlyHis 120
Db 326 GAGACGGGCTCGTATGCGAGGGCGCTGCTGAACTTCAAGGCTGCCCACTCAGGTAC 385
QY 121 LeuTyrAsnProMetSerIleGlyIleSerPheMetGlyAsnTyrMetAspArgValPro 140
Db 386 TTATGGAACCCCATGCTCATGTGGCATGCTTCACTGAGCACTACATGATGCGGTGCCC 445
QY 141 ThrProGlnAlaIleArgAlaAlaGlnGlyLeuLeuAlaCysGlyValAlaGlnGlyAla 160
Db 446 ACACCCCAAGCCGATCCGGGACGCGCAGGAGTCTACTGCGCTGCGGTGCTCAGGAGCC 505
QY 161 LeuArgSerAsnTyrValLeuTyrGlyHisArgAspValGlnArgThrLeuSerProGly 180
Db 506 CTGAGGTCCCACTATGTGCTCAAGAGACACCGGGATGTGACGATGACACTCTCTCCAGGC 565
QY 181 AsnGlnLeuTyrHisLeuIleGlnAsnTyrProHisTyrArgSerPro 196
Db 566 AACCACTCTACCACTCATCAGAAATGGCCACACTACCGCTCCCCC 613

RESULT 4
BD078857 718 bp DNA linear PAT 27-AUG-2002
LOCUS Tumor proliferation inhibition- and apoptosis-associated gene and
DEFINITION polyepptide and method of using the same.
ACCESSION BD078857
VERSION BD078857.1 GI:22624460
KEYWORDS JP 2001509384-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 718)

Db 330 GAAGACGGCTCGATATACGAGGCGCGTGGTCACTCAAGGATCCCACTCAGGTAC 389
Qy 121 LeuTrpAsnProMetSerIleGlyIleSerPheMetGlyAsnTyrMetAspArgValPro 140
Db 390 TTTATGAACTCCATGTCATTGGCATGAGCTTCACTGAGCACTACATGATCGCGTGGCC 449
Qy 141 ThrProGlnAlaIleArgAlaIleGlnGlyLeuLeuAlaCysGlyValAlaGlnGlyAla 160
Db 450 ACAACCCAGGCGCATCCGCGGAGCGCGGTCTACTGCGCTGCGGTGCTCAGGAGGCC 509
Qy 161 LeuArgSerAsnTyrValIleuLysGlyHisArgAspValGlnArgThrLeuSerProGly 180
Db 510 CTGAGGTCCACTATGTGTCTAAAGACACCGGATGTGACGCTACACTCTCTCCAGGC 569
Qy 181 AsnGlnLeuTyrHisLeuIleGlnAsnTyrProHisTyrArgSerPro 196
Db 570 AACCAAGCTTACCACTCCTCATCCAGAAATTGGCCACACTACCGCTCCCC 617

RESULT 6
BD261706
LOCUS 12 human secreted proteins. 726 bp DNA linear PAT 17-JUL-2003
DEFINITION BD261706
ACCESSION BD261706.1 GI:33071474
VERSION JP 2002530062-A/17.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 726)
AUTHORS Ni, J., Ruben, S.M., Olsen, H.S., Young, P.E., Kenny, J.D., Moore, P.A., Wei, Y.F. and Greene, G.M.
TITLE 12 human secreted proteins
JOURNAL Patent: JP 2002530062-A 17 17-SEP-2002;
HUMAN GENOME SCIENCES INC
COMMENT OS Homo sapiens (human)
PN JP 2002530062-A/17
PF 17-SEP-2002
PD 27-OCT-1999 JP 2000582421
PR 28-OCT-1998 US 60/105971
PI JIAN NI, STEVEN M RUBEN, HENRIK S OLSEN, PAUL E YOUNG, JOSEPH J KENNY,
PI PAUL A MOORE, YING FEI WEI, JOHN M GREENE
PC C12N15/09, A61K31/7088, A61K35/76, A61K38/00, A61K39/395, A61K48/00,
PC A61P3/10, A61P7/00, A61P9/06, A61P11/06, A61P17/02, A61P17/06,
PC 06, A61P19/02, A61P25/16, A61P25/18, A61P25/22, A61P25/24, A61P25/28,
PC A61P27/02, A61P27/06, A61P29/00, A61P29/00, A61P31/04, A61P31/18, A61P33/02,
PC A61P33/04,
PC A61P33/06, A61P35/00, A61P35/02, A61P37/02, A61P37/04, A61P37/06,
PC A61P43/00,
PC C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10 PC
PC C12P21/02, C12Q1/02,
PC C12Q1/68, G01N33/53, G01N33/566// (C12P21/02, C12R1:19), (C12P21/02, PC C12R1:19),
PC C12N15/00, C12N5/00, A61K37/02
CC 12 human secreted proteins
FH Key Location/Qualifiers
FT source 1..726
FT /organism="Homo sapiens (human)".
FT Location/Qualifiers
1..726
1..organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Pred. No.: 3,85e-93 Length: 726
Score: 1074.00 Matches: 196
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-015-390A-216 (1-196) x BD261706 (1-726)

Qy 1 MetSerArgGlySerMetLeuLeuAlaTrpAlaLeuProSerLeuLeuArgLeuGlyAla 20
Db 32 ATGTCCCGCCGCTCTATGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 91
Qy 21 AlagInGluTrpGluAspProAlaCysCysSerProIleValProArgAsnGluTrpLys 40
Db 92 GCTCAGAGACAGAGAGACCCGCTGCTGAGCCCATAGTGCCTGGAAAGAGTGAAG 151
Qy 41 AlaLeuAlaSerGluCysAlaGlnHisLeuSerLeuProLeuArgTyrValValValSer 60
Db 152 GCCCTGGCATCAGAGTGGCGCCAGACCTGAGCTGCTTACGCTATGTGTGTATCG 211
Qy 61 H1STRAlaGlySerSerCysAsnThrProAlaSerCysGlnGlnAlaArgAsnVal 80
Db 212 CACACGCGCGGAGAGAGCTGCAACACCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 271
Qy 81 GlnHisTyrHisMetIleThrLeuGlyTyrCysAspValGlyTyrAsnPheLeuIleGly 100
Db 272 CAGCACTACCATGATGAGACACTGGGCTGTGTGCGACGTGGGTACAACTTCTGTGATTGA 331
Qy 101 GluAspGlyLeuValTyrGluGlyValArgGlyTyrAsnPheTrpGlyAlaHisSerGlyHis 120
Db 332 GAAGACGGCTGTATACAGAGGCGGTGCTGGAATTCACGGGTGCCCACTCAGTAC 391
Qy 121 LeuTrpAsnProMetSerIleGlyIleSerPheMetGlyAsnTyrMetAspArgValPro 140
Db 392 TTTATGAACTCCATGTCATTGGCATGAGCTTCACTGAGCACTACATGATCGGTGCGCC 451
Qy 141 ThrProGlnAlaIleArgAlaIleGlnGlyLeuLeuAlaCysGlyValAlaGlnGlyAla 160
Db 452 ACAACCCAGGCGCATCCGCGGAGCGCGGTCTACTGCGCTGCGGTGCTCAGGAGGCC 511
Qy 161 LeuArgSerAsnTyrValIleuLysGlyHisArgAspValGlnArgThrLeuSerProGly 180
Db 512 CTGAGGTCCACTATGTGTCTAAAGACACCGGATGTGACGCTACACTCTCTCCAGGC 571
Qy 181 AsnGlnLeuTyrHisLeuIleGlnAsnTyrProHisTyrArgSerPro 196
Db 572 AACCAAGCTTACCACTCCTCATCCAGAAATTGGCCACACTACCGCTCCCC 619

RESULT 7
BD267640 749 bp DNA linear PAT 17-JUL-2003
LOCUS BD267640
DEFINITION Peptidoglycan recognition proteins.
ACCESSION BD267640.1 GI:33077408
VERSION JP 200253134-A/3.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 749)
AUTHORS Rosen, C.A., Ruben, S.M., Young, P.E. and Olsen, H.S.
TITLE Peptidoglycan recognition proteins
JOURNAL Patent: JP 200253134-A 3 08-OCT-2002;
HUMAN GENOME SCIENCES INC
COMMENT OS Homo sapiens (human)
PN JP 200253134-A/3
PF 08-OCT-2002
PD 22-DEC-1999 JP 2000591216
PR 23-DEC-1998 US 60/113809
PI CRAIG A ROSEN, STEVEN M RUBEN, PAUL E YOUNG, HENRIK S OLSEN PC C12N15/09, A61K31/7088, A61K38/00, A61P31/04, A61P31/12, PC A61P35/00,

FEATURES

source

ORIGIN

Alignment Scores.

Mon May 17 11:03:28 2004

us-10-015-390a-216.rge

Page 6

```

PC A61K35/04,A61P37/02,A61P43/00,C07K14/47,C07K16/18,C12N1/15,PC
C12N1/19,
PC
C12N1/21,C12N5/10,C12P21/02,C12Q1/02,C12Q1/68,G01N33/15,G01N33/PC
50,
PC G01N33/53,G01N33/53,G01N33/56,C12N15/00,C12N5/00,A61K37/02 CC
Peptidoglycan recognition proteins
FH Key location/Qualifiers
FT source 1..749
location/Qualifiers
location/Qualifiers
1..749
location/Qualifiers
1..749
/organism='Homo sapiens (human)'.
FEATURES
source
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'

```

Alignment Scores:	
Pred. No.:	3,39e-93
Score:	1074.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
GB:	6
Length:	749
Matches:	166
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-10-015-390A-216 (1-196) X BD267640 (1-749)

QY	1	MetSerIaGdAgSseMetLeuLeuAaIaTPhaIaLeuProSerLeuLeuAaGluGlyAa	20
Db	55	ATGTCGCCCGCTCTATGCTGCTGGCTGGGCTCTCCAGGCTCTCTTGATCTGGAGCG	114
QY	21	AlaGlnGluTnThGluAspProIaCysCysSerProIleValProArgSngIuTPhyS	40
Db	115	GCTCAGGAGACAGAAAGACCCGGGCTGCTGCACCCCAATGTCGCCGAGACAGTGGAA	174
QY	41	AlaLeuAlaSerGluCysAlaGlnHisLeuSerLeuProLeuArgTyValValAlaSer	60
Db	175	GCCCTGGCATCAGAGTGCGCCAGACCTGACCTGCTTACGCTATATGTGTGTATCG	234
QY	61	HisThrAlaGlySerSerCysAsnThrProAlaSerCysGlnGlnIaIaArgAsnVal	80
Db	235	CACAGGGCGGGAGCAGCTGCACAAACCCCGCTCTGTCAGAGAGAGACGCCGGAATGTG	294
QY	81	GlnHisTyHISMetIysThrLeuGlyTTPCysAspValGlyTyraAspHeuLeuIleGly	100
Db	235	CAGCACTACCAATGAGACATCTGGGCTGTGTGCGAGTGGCTACAACTTCTCGATTGGA	354
QY	101	GluAspGlyLeuValTyGluGlyArgGlyTPaAsnPheThrGlyAlaHisSerGlyHis	120
Db	355	GAAAGCGGGCTGTAATACAGAGGCGCTGCTGGAACTTACAGGGGTCCCACTCAGGTCAC	414
QY	121	LeuTPaAsnProMetSerIleGlyIleSerPheMetGlyAsnTyMetAspArgValPro	140
Db	415	TTATGGAAACCCCATGTGCATTGGCAATCAGCTTATATGGCACTACATGGATCGGGTGGCC	474
QY	141	ThrProGlnAlaIleArgAlaAlaGlnGlyLeuLeuAlaCysGlyValAlaGlnGlyAla	160
Db	475	ACACCCCAAGGCCATCCGGGAGGCCAGGGGTCTACTGGCTGGGTGTGGTCAAGGAGCC	534
QY	161	LeuArgSerAsnTyValLeuIleGlyHisHisArgAspValGlnArgThrLeuSerProGly	180
Db	535	CTGAGGTCCACTATGTGCTCAAGGACACGGGAAATGTGACAGGTCACACTCTCCAGGC	594
QY	181	AsnGlnLeuTyHisLeuIleGlnAsnTProHisTyraArgSerPro	196
Db	595	AACCAAGTCTACACCTCATCCGAATTTGGCCACACTACAGGCTTCCCC	642

RESULT 8	749 bp	DNA	1 linear	PAT 20-DEC-2002
AR226480				
LOCUS	AR226480			
DEFINITION	Sequence 5 from patent US 6444790.			
ACCESSION	AR226480			
VERSION	AR226480.1	GI:27265028		

```

KEYWORDS
SOURCE      Unknown.
ORGANISM     Unknown.
              Unclassified.
REFERENCE    1 (bases 1 to 749)
AUTHORS      Young, P.E., Ruden, S.M., Rosen, C.A. and Olsen, H.S.
TITLE        Peptidoglycan recognition proteins
JOURNAL      Patent: US 6444790-A 5 03-SEP-2002;
              Location/Qualifiers
FEATURES
             source
               1..749
               /organism="Unknown"
               /mol_type="genomic DNA"

```

```

Alignment Scores:
Pred. No.:      3,39e-93      length:      749
Score:          1074.00      Matches:     166
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches:  0
Query Match:    100.00%      Indels:      0
DB:              6          Gaps:         0
US-10-015-390A-216 (1-186) x AR226480 (1-749)

```

US-10-015-390A-216 (1-196) X AR226480 (1-749)

QY 1 MetSerArgArgSerMetLeuLeuAlaTrpAlaLeuProSerLeuLeuAlaGluAla 20
 Db 55 ATGTCCCGCGGCTCTGTGCTGTCCCGGGCTCTCCCAAGCTCTTCACTGGAGCG 114
 QY 21 AlAGlGluLThrGluAspProAlaCysCysSerProIleValProArgAnGluTrpLys 40
 Db 115 GCTAGAGAGACAGAAACCCCGGCTGTCTGACCCCAATGAGCCCGGAAAGAGTGGAG 174
 QY 41 AlaLeuAlaSerGluCysAlaGlnHisLeuSerLeuProLeuArgLysValValSer 60
 Db 175 GCCTGGCCATCAAGTGGCGGCCGAGCACTGAGCCTGACCTTAACCTTATGTGGTGTATCG 234
 QY 61 HisThrAlaGlySerSerCysAsnThrProAlaSerCysGlnGlnGlnAlaArgAsnVal 80
 Db 235 CACACGCGCGGCGAGCGCTGCACACCCCGCTGTCTCCAGCAGACAGGCCCGGAAGTGG 294
 QY 81 GlnHisThrHisMetLeuThrLeuGluLysTrpCysAspValGlyTyrAsnPhaLeuIleGly 100
 Db 295 CAGACCTACACATGAAGACACTGGGCTGTGTGCGACGTGGGCTCAACTTCTGATTGGA 354
 QY 101 GluAspGlyLeuValTyrGlnGlyLysArgLysTyrProAsnPhaThrGlyAlaHisSerGlyHis 120
 Db 355 GAACACGGGCTCGTATTCAGAGGGCCGTGTGCTGAACCTCACGGGTGGCCACTTCAGGTAC 414
 QY 121 LeuTrpAsnProMetSerIleGlyIleSerPheMetGlyAsnTyrMetAspArgValPro 140
 Db 415 TTATGGAAACCCCAATGCTCATGGAGCACTTCATGGGCACTACATGATCGGGTGGCC 474
 QY 141 ThrProGlnAlaIleArgAlaAlaGlnGlyLeuLeuAlaCysGlyValAlaGlnGlyAla 160
 Db 475 ACACCCCAGGCGAATCGGGGAGGCCCAAGGGCTACTGCTGTGGGTGGTCAAGGAGCC 534
 QY 161 LeuArgSerAsnTyrValLeuLysGlyHisAlaGlyAspValGlnArgThrLeuSerProGly 180
 Db 535 CTGAGAGTCCAACTATGTGCTCAAGAGCACCGGGAGTGCACAGCTCACTCTTCCAGGC 594
 QY 181 AsnGlnLeuTyrHisLeuIleGlnAsnTyrProHisTyrArgSerPro 196
 Db 595 AACCAAGCTCTACCACTTCATCCAAATGGCACTTACCGCTCCGCC 642

RESULT 9			
AX778312			
LOCUS	AX778312	537 bp	linear
DEFINITION	Sequence 469 from Patent WO03039443.		
ACCESSION	AX778312		
VERSION	AX778312.1	GI:32695306	
KEYWORDS			
SOURCE	Homo sapiens		
ORGANISM	Homo sapiens (human)		

REFERENCE
AUTHORS
TITLE
JOURNAL

1
Hafnerlach, T., Schoch, C., Kern, W., Kohlmann, A., Schmittger, S.,
Dugas, M., Ellis, R., Biers, B. and Mergenthaler, S.
Novel genetic markers for leukemias
Patent: WO 03039443-A 469 15-MAY-2003;
Deutsches Krebsforschungszentrum (DB) ;
Ludwig-Maximilians-Universität München
PD Dr. Dr. (DE) ; Schoch, Claudia (DE) ; Kern, Wolfgang (DE)

FEATURES
source
1..537
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Alignment Scores:
Pred. No.: 3,46e-85 Length: 537
Score: 989.00 Matches: 179
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 92.09% Indels: 0
DB: 6 Gaps: 0

US-10-015-390A-216 (1-196) x AX778312 (1-537)

QY 16 LeuHrGlenglylaalaingluThrGluAspProAlaCysCysSerProIleValPro 35
DB 1 CTTCGACTCGAGGCGCTCAGAGACAGAAAGCCGGCGCTGCGACACCCCATATGCCCC 60
QY 36 ArgAsnGluTrpLysAlaLeuAlaSerGluCysAlaGlnHisLeuSerLeuProLeuArg 55
DB 61 CGGAACGAGTGAAGGCGCTGCGATCAGAGTGGCGCCAGACCTGAGCTGCTTACGC 120
QY 56 TyrValValAlaSerHisThrAlaGlySerSerCysAsnThrProAlaSerCysGlnGln 75
DB 121 TATGTGTGTATGCGACACGCGCGGACAGCGACACCCCGCTGTGTCCAGCAG 180
QY 76 GlnAlaArgAsnValGlnHisTyrHisMetCysThrLeuGlyTrpCysAspValGlyTyr 95
DB 181 CAGGCCCGGANTGCGACGACTACCATGAAGCACTGGGCTGTGTCCAGCTGGCTAC 240
QY 96 AsnPhenIleGlyGluAspGlyLeuValTyrGluGlyTyrPheAsnPhenGly 115
DB 241 AACTTCTGATTGAGAGAGCGGCTGTATACAGAGGCGCTGGAATCTTACAGCGGT 300
QY 116 AlaHisSerGlyHisLeuTrpAsnProMetSerIleGlyIleSerPheMetGlyAsnTyr 135
DB 301 GCCCACTCAGGCTCATATGAGACCCCATGTCCATTCGACTCAGCTTCAAGGGCACTAC 360
QY 136 MetAspArgValProThrProGlnAlaIleArgAlaIleGlnGlyLeuLeuAlaCysGly 155
DB 361 ATGATCGGGTGGCCACACCCCGACCATCCGGGACGAGGCTTACTAGCGGT 420
QY 156 ValAlaGlnGlyAlaLeuArgSerAsnTyrValLeuGlyGlyHisAspAspValGlnArg 175
DB 421 GTGGCTCAGGAGCGCTGAGGTCCAACTATGTCTCAAGAGACCCGGGATGTGACAGGT 480
QY 176 ThrLeuSerProGlyAsnGlnLeuTyrHisLeuIleGlnAsnTyrProHisTyrArg 194
DB 481 ACACTCTCCAGGACACCACTCTACCACTCACTCAAGAAATGGCCACACTACCGC 537

RESULT 10
CDRI31676 700 bp mRNA linear MAM 21-DEC-2000
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CDRI31676 700 bp mRNA linear MAM 21-DEC-2000
Camelus dromedarius mRNA for peptidoglycan recognition protein.
AJ31676.1 GI:11990123
peptidoglycan recognition protein.
Camelus dromedarius (Arabian camel)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

1
Kappeler, S.R., Farah, Z. and Puhar, Z.
Milk as a Source of Camel (Camelus dromedarius) Peptidoglycan
Recognition Protein
Unpublished
2 (bases 1 to 700)
Kappeler, S.R.
Direct Submission
Submitted (21-DEC-1998) Kappeler S.R., Institute of Food Science,
Swiss Federal Institute of Technology, LFO F26, 8092 Zurich,
SWITZERLAND

FEATURES
source
1..700
Location/Qualifiers
/organism="Camelus dromedarius"
/mol_type="mRNA"
/sub_species="Somali breed"
/db_xref="taxon:9838"
/tissue_type="lactating mammary gland"
25..606
/codon_start=1
/product="peptidoglycan recognition protein"
/protein_id="CAC19553.1"
/db_xref="GI:11990124"
/db_xref="GOA:Q9GK12"
/db_xref="SPTREMBL:Q9GK12"
/translation="MTRACVLVVALALLSLGAREDDPACGSIVPEREWALASEC
RELRPRVYVSHRAGHCDTPACQAOQONVSYVRLGCDVYNLLIEDGL
VYEGRWIKAHAGAPTRPISIGISPMGNMNPVPRALRAQNLACGVALGALR
SNTEVGRHVDQPTSPEDRKEIITWSHRA"

CDS

sig_peptide
mat_peptide
polYA_signal
Alignment Scores:
Pred. No.: 2,47e-65 Length: 700
Score: 782.00 Matches: 142
Percent Similarity: 84.10% Conservative: 22
Best Local Similarity: 72.82% Mismatches: 29
Query Match: 72.81% Indels: 2
DB: 4 Gaps: 1

ORIGIN

US-10-015-390A-216 (1-196) x CDRI31676 (1-700)

QY 1 MetSerArgArgSerMetCysLeuAlaLeuProSerLeuLeuArgGluGlyAla 20
DB 25 ATGACCCCGGCACTGGGTGTTCTCGTGGGCTTCCGCGCTCCTCAGCCTCGAGCG 84
QY 21 AlaGlnGluThrGluAspProAlaCysCysSerProIleValProArgAsnGluTrpLys 40
DB 85 GCTCGA-----GAAGACCCCGCGCGCTGCGCTCCATGTGCTCCGAGAGAGG 138
QY 41 AlaLeuAlaSerGluCysAlaGlnHisLeuSerLeuProLeuArgTyrValValAlaSer 60
DB 139 GCCCTGGCGCTCCGAGTGCAGAGAAAGCTTAACACGCGCGGTGCTAGTGTGTGTCG 198
QY 61 HisThrAlaGlySerSerCysAsnThrProAlaSerCysGlnGlnGlnAlaArgAsnVal 80
DB 199 CACACTGCGCGGACGACACGCGACACCCGCGCTTGTGTGCGCGACAGCCCGAGACGTG 258
QY 81 GlnHisTyrHisMetCysThrLeuGlyTrpCysAspValGlyTyrAsnPhenIleGly 100
DB 259 CAAAGCTTACATGTGCGGAACCTGGGCTGTGTGCGACGTGGCTTCACTTCTGATCGGA 318
QY 101 GluAspGlyLeuValTyrGluGlyTyrPheAsnPhenThrGlyAlaHisSerGlyHis 120
DB 319 GAAAGATGGGCTGTGTGACGAAAGCGGAGCTGGAACATCAAGGCGCCACGAGGTCCC 378
QY 121 LeuTrpAsnProMetSerIleGlyIleSerPheMetGlyAsnTyrMetAspArgValPro 140
DB 379 ACTTGAACCCCATATCCATAGGCACTTCTTCAAGGCGACATATGATGAGTGGCC 438


```
/profile_id="AAP060335.1"
/db_xref="GI:6273361"
/translation="MLPACALLALLGLATSCFTYDRSEWRALPSECGSRILGHPRVYV
VISHASFGNCSPGSCQQAQAVNQHYNKELGCDVAYNFLGEGGHYERGGNNIKG
DHGIGWNPSSGILTPNGGMDRPAKRAARALNLGCGVSRGLRANVEYKGRDQV
OSTSPEDQLYQVITQSWENHRE"
```

ORIGIN

Alignment Scores:	
Pred. No.:	3,668-57
Score:	696.00
Percent Similarity:	78.4%
Best Local Similarity:	67.3%
Query Match:	64.80%
DB:	10
Length:	669
Matches:	128
Conservative:	21
Mismatches:	33
Indels:	1
Gaps:	1

US-10-015-390A-216 (1-196) X AF193843 (1-669)

Oy	5	SerMetLeuLeuAlaTrpAlaLeuProSerLeuLeuArgLeuGlyAlaAlaGlnGluThr	24
Db	22	AGCATGTGTGTTGGCTGTGCTCTCTTGGCCCTCGGGCTGGCAACTCC-----	72
Oy	25	GluAspProAlaCysCysSerProIleValProArgAsnGluTrpLysAlaLeuAlaSer	44
Db	73	-----TGCAGTTTATCGTGCCCGGCACTGAGTGGAGGGCCCTGGCATTCC	117
Oy	45	GluCysAlaGlnHisLeuSerLeuProLeuArgIlyValValSerHisThrAlaGly	64
Db	118	GAGTCTCTAGACCGGCTGGGGCACCAGATCCGCTGCTGATCTCCACACAGCCGGC	177
Oy	65	SerSerCysAsnThrProAlaSerCysGlnGlnGlnAlaArgAsnValGlnHisThrHis	84
Db	178	AGCTTCTGCAAGGCGCGGACTCTCGTGAACAGCAGCGCCGGAATGTGGACATTACAC	237
Oy	85	MetIlyThrLeuGlyTrpCysAspValGlyIlyrAsnPhaLeuIleGlyGluAspLysLeu	104
Db	238	AAGATGAGCTGGCGGTGGCGCATGAGCTTCAACTTCTATTGAGAGGAGCGGTAT	297
Oy	105	ValIlyrGlnGlyArgGlyTyrAsnPhaThrGlyAlaHisSerGlyHisLeuThrAsnPro	124
Db	298	GCTCTGGAAGCGCCGAGCGCGAATCAAGAGGTGACACACAGGCGCCATCTGGAAATCCC	357
Oy	125	MetSerIleGlyIleSerPheMetGlyAsnTyrMetAspArgValProThrProGlnIle	144
Db	358	AGGTCTATTGGGATCATCCTTCATGGGGAACTTCATGAGACGGGGTACCCGCAAGCGGGCC	417
Oy	145	IleArgAlaAlaGlnGlyLeuLeuAlaCysGlyValAlaGlnGlyValaLeuArgSerAsn	164
Db	418	CTTCGCTGCTGCCCTTAATCTTCTGGAAATGTGGGGTGTCTCGGGGCTTCTCTGAGATCCAA	477
Oy	165	IlyrValLeuLysGlyHisIleArgAspValGlnArgThrLeuSerProGlyAsnGlnLeuTyr	184
Db	478	TATGAGATCAAGAGCACCGGGATGTGGCAAAACACTCTCTTCACAGTGAACCAACTGTAT	537
Oy	185	HisLeuIleGlnAsnTyrProHisTyrArg	194
Db	538	CAGGTCTATCAAGAGCTGGGAACTTACCGCA	567

RESULT 13

LOCUS	AF076482	680 bp	mRNA	linear	ROD 15-AUG-1998
DEFINITION	Mus musculus neotidocyan recognition protein precursor (Pam)				

DEFINITION Mus musculus peptidoglycan recognition protein (vgp) mRNA, complete cds.

ACCESSION AF076482
LIBRARY AF076482 1 CT-3343530

AF076482.1 GI:3342530

SOURCE	Mus musculus (house mouse)
1	
2	
3	
4	
5	
6	
7	
8	
9	
10	
11	
12	
13	
14	
15	
16	
17	
18	
19	
20	
21	
22	
23	
24	
25	
26	
27	
28	
29	
30	
31	
32	
33	
34	
35	
36	
37	
38	
39	
40	
41	
42	
43	
44	
45	
46	
47	
48	
49	
50	
51	
52	
53	
54	
55	
56	
57	
58	
59	
60	
61	
62	
63	
64	
65	
66	
67	
68	
69	
70	
71	
72	
73	
74	
75	
76	
77	
78	
79	
80	
81	
82	
83	
84	
85	
86	
87	
88	
89	
90	
91	
92	
93	
94	
95	
96	
97	
98	
99	
100	

ORGANISM

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE AUTHORS

JOURNAL MEDLINE
FROM INSECTS TO HUMANS
PROC. NATL. ACAD. SCI. U.S.A. 95 (17), 10078-10082 (1998)
98374308
PUBMED
9707603
2 (Baes 1 to 680)
Kang, D., Liu, G., Lundstrom, A., Gelius, E. and Steiner, H.
Direct Submission
Submitted (08-JUL-1998) Microbiology, Stockholm University

FEATURES
SOURCE

gene
CDS

genes

ORIGIN

Alignment Scores:	
pred. No.:	3,75e-57
Score:	695.00
Percent Similarity:	78.42%
Best Local Similarity:	67.37%
Query Match:	64.80%
DB:	10
Length:	680
Matches:	128
Conservative:	21
Mismatches:	33
Indels:	9
Gaps:	1

US-10-015-390A-216 (1-196) X AF076482 (1-680)

```

QY      5 SerMetLeuLeuAlaATPrAlaLeuProSerLeuLeuArgLeuGlyAlaAlaGlnGluThr 24
Db      33 AGCAGTGTGTGGCTGTGCTCTCTCTGCTCCCTCCGGCTCGGCACCTCC----- 83
QY      25 GluAepProAlaCysCysSerProIleValProArgAsnGluTyrPylAsAlaLeuAlaSer 44
Db      84 -----TGCAGTTTCATCTGTGCCCGCAGTAGTAGGAGGCGCTGCATCC 128
QY      45 GluCysAlaGlnHisLeuSerLeuProLeuArgTyrValValValSerHisThrAlaGly 64
Db      129 GAGTGTCTTAAGCCGCGCTGGGCATTCACATTCGCTACGCTGATCTCCACACACACCGGC 188
QY      65 SerSerCysAsnThrProAlaSerCysGlnGlnGlnAlaArgAsnValAlaHisTyrHis 84
Db      189 AGCTTCTGCACACAGGCCGAGCTCCGTGTAAACAGCAGGCCCGCATGTGCAGATTACCAAC 248
QY      85 MetIlyThrLeuGlyTyrCysAspValGlyTyrAsnPhaLeuIleGlyGluAepGlyLeu 104
Db      249 AAGATGACGTGGCGCTGTGCGATGTACGCTTCAACTTCCTTATTGAGAGAGACGGTCAT 308
QY      105 ValTyrGlnGlyArgGlyTyrAsnDheThrGlyAlaHisSerGlyHisLeuTyrAsnPro 124
Db      309 GTCATTGAAGGCCGAGGCTGCACATCAAGGGTGCACACAGGCCCATCTGCAATCCC 368
QY      125 MetSerIleGlyIleSerPheMetGlyLeuTyrMetLapArgValProThrProGlnAla 144
Db      369 AAGTCTATTGGCATCACTTCATGGGGAATTCATAGACCGGGTACCCGCAAGCGGGCC 428

```

Oy		145	IL6ARALAI GLINGLYEULEULAEYGLIYALIALINLIYALIEURGERSEN	164
Dd		429	CTCGGTCGCCCTAAATCTTCTGGGAAGTGCGGTGTCGCGGCCTTCCTGACATCCAAC	488
Oy		165	TyrValLeuIleuYGlyYHISrGAsrYaGIlnrhGrHeuseerProclYasntInleYr	184
Dd		489	IATGAAGTCAAAAGGACACCAGGATGTGGAAAGCATCTCTCTCCAAAGTAACAACACTAT	548
Oy		185	HISLeuIIeGIlnAsnTrPProHISrTYArG	194
Dd		549	CAGGTGATCCAAGCTGGAGCACATACACGA	578
RESULT 14				
LOCUS	BC005582			
DEFINITION	Mus musculus peptidoglycan recognition protein, mRNA (cdna clone			
ACCESSION	BC005582			
VERSION	MG005582.1			
KEYWORDS	GI:13542755			
SOURCE	MG005582.1			
ORGANISM	Mus musculus (house mouse)			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.			
	1 (bases 1 to 713)			
	Klausner,R.D., Collins,F.S., Wagner,L.H., Derge,J.G.,			
	Altshuler,S.F., Zeeberg,B., Buecok,K.H., Schaefer,C.F., Bat,N.K.,			
	Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,Y., Hasleh,F.,			
	Diachenko,L., Martinska,K., Farmer,A.A., Rubin,G.M., Hong,L.,			
	Shapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,			
	Scheetz,T.E., Brownstein,M.J., Udell,T.B., Teshiyuki,S.,			
	Cernici,P., Prange,C., Rana,S.S., Loquellano,N.A., Peters,G.J.,			
	Adrianson,R.D., Mullany,S.U., Bosk,S.A., McEwan,P.U.,			
	McKernan,K.C., Hale,S., Garcia,A.M., Gay,L.J., Richards,S.,			
	Vallilon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,			
	Fahney,J., Helton,E., Kettelman,M., Madan,A., Rodgers,S.,			
	Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,			
	Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,			
	Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,			
	Butterfield,Y.S., Krzywicki,M.T., Skalski,U., Smalley,D.B.,			
	Scherzer,A., Schein,J.E., Jones,V., and Marra,M.A.			
	Generation and initial analysis of more than 15,000 full-length			
	human and mouse cDNA sequences			
	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)			
TITLE	2 (bases 1 to 713)			
JOURNAL	Straussberg,R.			
MEDLINE	Direct Submission			
PUBMED	Submitted (02-Apr-2001) National Institutes of Health, Mammalian			
REFERENCE	Gene Collection (MGC), Cancer Genomics Office, National Cancer			
AUTHORS	Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,			
TITLE	USA			
JOURNAL	NIH-MGC Project URL: http://mgc.nci.nih.gov			
	Contact: MGC help desk			
	Email: cgabs-remail.nih.gov			
	Tissue Procurement: Gilbert Smith, Ph.D.			
	cDNA Library Preparation: Life Technologies, Inc.			
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)			
	Sequencing Center			
	Center code: BCM-HGSC			
	Web site: http://www.hgsc.bcm.tmc.edu/cdna/			
	Contact: amg@bcm.tmc.edu			
	Gunaratne, P.H., Garcia, A.M., Lu, X., Huiyk, S.W., Loulseseg, H.,			
	Kowitz, C.R., Speed, A.U., Martin, R.G., Muzny, D.M., Natarati,			
	A.N., Gibbs, R.A.			
REMARK	Clone distribution: MGC clone distribution information can be found			
COMMENT	through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov			

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6679292.

Location/Qualifiers

1..713

/organism="Mus musculus"

/mol_type="mRNA"

/strain="FVB/N"

/db_xref="taxon:10090"

/clone="MGC:11430 IMAGE:3969014"

/tissue_type="mammary tumor, Metallothionien-TGF alpha model, 10 month old virgin mouse. Taken by biopsy."

/clone_1ib="NCI CGAP_Mam1"

/lab_host="MDH10B"

/note="vector: pCMV-SportC"

1..713

/gene="Pglyrp"

/note="Synonyms: PGRP, Tag7, PGRP-L, PGRP-S"

/db_xref="locusid:21946"

/db_xref="MG1:1345092"

47..595

/codon_start=1

/product="Pglyrp protein"

/protein_id="AA05582.1"

/db_xref="ngi:13542756"

/db_xref="locusid:21946"

/translation="MELPACALVALGLATSCFFYPRSEMRALPECCSRIGHPVRIVVISHSRSPCNPSDSCQARNVQHAKRELQMCVVAANFLIGEGHYEERGNINNGDHTEGNNPMPSIGITTFWGNFMEDRVPAKRALRALNMLRGVSRLRENTYVKGRADVSTLSPDPOLIQVYQSSEHRE"

107..529

/note="PGRP: Region: Animal peptidoglycan recognition proteins homologous to bacteriophage T3 lysozyme. The bacteriophage molecule, but not its moth homologue, has been shown to have N-acetylmuramoyl-L-alanine amidase activity. One member of this family, Tag7, is a cytokine"/db_xref="CDD:smart00701"

misc_feature

/note="PGRP: Region: Animal peptidoglycan recognition proteins homologous to bacteriophage T3 lysozyme. The bacteriophage molecule, but not its moth homologue, has been shown to have N-acetylmuramoyl-L-alanine amidase activity. One member of this family, Tag7, is a cytokine"/db_xref="CDD:smart00701"

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:
3..95e-57	696.00	713	128
Percent Similarity:	78.42%	Conservative:	21
Best Local Similarity:	67.37%	Mismatches:	33
Query Match:	64.80%	Gaps:	8
DB:	10	gaps:	1

US-10-015-390A-216 (1-196) x BC005582 (1-713)

Cy	5	SerMetLeuLeuAlaTrpAlaLeuProSerLeuLeuArgLeuGIValalaInglunthr	24
Db <td>44</td> <td>AGCATGTCTTGGCTCGTCGCTCTCTGCCCTCTGGCAACTCC-----</td> <td>94</td>	44	AGCATGTCTTGGCTCGTCGCTCTCTGCCCTCTGGCAACTCC-----	94
Cy <td>25</td> <td>GIUasrProAlaCyS CySerProIleValProArAsnGlutTPLYeaAlaEuLaSer</td> <td>44</td>	25	GIUasrProAlaCyS CySerProIleValProArAsnGlutTPLYeaAlaEuLaSer	44
Db <td>95</td> <td>-----TGCAATTTCATGTCGCCCGGACGAGAGGAGGAGGCGCTGCCATCC</td> <td>139</td>	95	-----TGCAATTTCATGTCGCCCGGACGAGAGGAGGAGGCGCTGCCATCC	139
Cy <td>45</td> <td>GIUCyAlaGlnHisLeuSerLeuProLeuArgTYVaIValValSerHisThrZlaGIY</td> <td>64</td>	45	GIUCyAlaGlnHisLeuSerLeuProLeuArgTYVaIValValSerHisThrZlaGIY	64
Db <td>140</td> <td>GAGTGTCTACGCCGCTGGGCAACCAGTTCCGTAAGTGTATCTCACACAACCGGAC</td> <td>199</td>	140	GAGTGTCTACGCCGCTGGGCAACCAGTTCCGTAAGTGTATCTCACACAACCGGAC	199
Cy <td>65</td> <td>SerSerCyAsenThPrroAlaSerCyGingInGIAlaAsnValaGlnHisTyrtis</td> <td>84</td>	65	SerSerCyAsenThPrroAlaSerCyGingInGIAlaAsnValaGlnHisTyrtis	84
Db <td>200</td> <td>AGCTTGTGAAGGCCGCACTCTGTGAACAGAGGAGCGGCAATGTGASCATTAACAC</td> <td>259</td>	200	AGCTTGTGAAGGCCGCACTCTGTGAACAGAGGAGCGGCAATGTGASCATTAACAC	259
Cy <td>85</td> <td>MeTlysThrLeuGIYTrPCyAspValGIYTYrasPhelenuIecYGIUaspLIyeu</td> <td>104</td>	85	MeTlysThrLeuGIYTrPCyAspValGIYTYrasPhelenuIecYGIUaspLIyeu	104
Db <td>260</td> <td>AAGAATGAGCTGGCTGGTGGATGTAGTACCAACTTCCTTATTGAGAGGACGTCAT</td> <td>319</td>	260	AAGAATGAGCTGGCTGGTGGATGTAGTACCAACTTCCTTATTGAGAGGACGTCAT	319
Cy <td>105</td> <td>VAlTYrGIUGIAYrGIYTrAsnPhethnGIValHisSerGIYHisneutTPsnPro</td> <td>124</td>	105	VAlTYrGIUGIAYrGIYTrAsnPhethnGIValHisSerGIYHisneutTPsnPro	124
Db <td>320</td> <td>GTCTATTGAAGGCCGCTGGAACATCAAGGATGACACACAGGCGCCACTGTGAATCCC</td> <td>379</td>	320	GTCTATTGAAGGCCGCTGGAACATCAAGGATGACACACAGGCGCCACTGTGAATCCC	379

Mon May 17 11:03:28 2004

us-10-015-390a-216.rge

Page 11

[illegible]

Ox 146 ATGATAAAGTGGCTGTCTTGGAATGCGGGGCTTCCTGAGTCCAACTAT 456
Db 397 CCGCGCCGCCCTAAATCTTCTTGGAATGCGGGGCTTCCTGAGTCCAACTAT 456

Cy 166 ValLeuIysGlyHisArgPheValGlnArgThrLeuSerProGluYasnGlnLeuThrs 188
Db 457 GAAAGTCAAAGACACCGGAGTGTGCAAAAGCACTCTCTCCAGGTGACCAACTATCAG 516

Ox 186 LeuIleGlnAsnTrpProHisIstfYarg 194
Db 517 GTCATCCCAAGCTGGGAAACAACACCA 543

Search completed: May 16, 2004, 18:33:09
Job time : 3731 secs

RESULT 15			
AR124884			
LOCUS	AR124884	549 bp	DNA
DEFINITION	Sequence 1 from patent US 6172211.		linear
ACCESSION	AR124884		
VERSION	AR124884.1	GI:14110245	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 549)		
AUTHORS	Georgiev,G.P., Kiselev,S.L., Prokhorchouk,E.B. and Ostermann,E.		
TITLE	Nucleic acid encoding tag7 polypeptide		
JOURNAL	Patent: US 6172211-A 1 09-JAN-2001;		
FEATURES	Location/Qualifiers		
source	1..549		

ORIGIN

Alignment Scores:	
Pred. No.:	7,14-57
Score:	692.00
Percent Similarity:	78.31%
Best Local Similarity:	67.40%
Query Match:	64.43%
DB:	6
Gaps:	1
Length:	549
Matches:	127
Conservative:	21
Mismatches:	33
Indels:	8
Gaps:	1

US-10-015-390A-216 (1-196) X AR124884 (1-549)

[illegible]

```

126 SerIleGlyIleSerPheMetGlyAsnTyrMetAspArgValProThrProGlnAlaIle 145
|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
337 TCTATTGCATCACTTCATGGGGACTTCATGGACCGGGGTACCCGCAAGCGGGCCCTC 396

```


SOURCE ORGANISM	
Homo sapiens (human)	
Homo sapiens	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
1 (bases 1 to 697)	

REFERENCE

1. (bases 1 to 697)

Clark, H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J., Chen, T., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B.,

Dowd, P., Bacon, D., Foster, J., Grimaldi, C., Gu, Q., Hass, P. E.,
Heldens, S., Huang, A., Kim, H. S., Klimowski, L., Jin, Y., Johnson, S.,
Lee, J., Lewis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C.,
Schaefer, J., Seshadri, S., Simmons, L., Sindt, J., Smith, V.,

TITLE	Author(s)
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins:	Xie, M.H., Yamasaki, D., Xie, Y., Gu, H., Huang, C., Zhang, W., Zhang, B., Goddard, A., Wood, W.I., and Goddard, P.

**JOURNAL OF
Genome Res. 13 (10), 2265-2270 (2003)**

PUBLISHED 129/3309
REFERENCE 2 (pages 1 to 697)

AUTHORS
 TITLE
 Direct Submission

JOURNAL
SUBMITTED (VI-ABS-2003) DEPARTMENT OF
INC. 1 DNA Way, South San Francisco, CA 94080, USA

REMOVED
SOURCE
1. .697

```

/mol_type="mRNA"

```

```
/clone="DNA66520"
```

```
/locus_tag="UNQ639"
```

```
/locus_tag="UNQ639"
```

```
/codon_start=1
```

```
/protein_id="AAQ89295.1"
```

```
/translation="MSRRSMLLAWALPSLRLTGAAQETEDPACCSPIVPRNEWKALAL
```

GLVYEGRGWFTGAHSGHLWNPMSIGISFMGNYMDRAVEIPQAIKAAQGELACGVADGR
TDAATTCACUUDYOBETSPGNOLYHIIONWBHYRSP"

ORIGIN

Query Match	Score 697;	DB 9;	Length 697;
100.0%;			
100.0%;	Pred NC 1-2e-143;		

Matches	697;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
---------	------	--------------	----	------------	----	--------	----	------	----

[illegible]

Dd 1 TCCCGACCTTGGCCGCTGCCAIAIGCCTGCCTCAAGATTC

61 CCCCAGCCCTCTCGACCTGGAGCCTGCTATGGTAACTATTATTAATTT
QY

b1 CCCCAGCCICCIIGACIIGGCGGGCAGCACGCCTTGTTC

b6
b7c

127 CHAIRS

128

129

130

131

132

133

134

135

136

137

138

139

140

141

142

143

144

145

146

147

148

149

150

151

152

153

154

155

156

157

158

159

160

161

162

163

164

165

166

167

168

169

170

171

172

173

174

175

176

177

178

179

180

181

182

183

184

185

186

187

188

189

190

191

192

193

194

195

196

197

198

199

200

201

202

203

204

205

206

207

208

209

210

211

212

213

214

215

216

217

218

219

220

221

222

223

224

225

226

227

228

229

230

231

232

233

234

235

236

237

238

239

240

241

242

243

244

245

246

247

248

249

250

251

252

253

254

255

256

257

258

259

260

261

262

263

264

265

266

267

268

269

270

271

272

273

274

275

276

277

278

279

280

281

282

283

284

285

286

287

288

289

290

291

292

293

294

295

296

297

298

299

300

301

302

303

304

305

306

307

308

309

310

311

312

313

314

315

316

317

318

319

320

321

322

323

324

325

326

327

328

329

330

331

332

333

334

335

336

337

338

339

340

341

342

343

344

345

346

347

348

349

350

351

352

353

354

355

356

357

358

359

360

361

362

363

364

365

366

367

368

369

370

371

372

373

374

375

376

377

378

379

380

381

382

383

384

385

386

387

388

389

390

391

392

393

394

395

396

397

398

399

400

401

402

403

404

405

406

407

408

409

410

411

412

413

414

415

416

417

418

419

420

421

422

423

424

425

426

427

428

429

430

431

432

433

434

435

436

437

438

439

440

441

442

443

444

445

446

447

448

449

450

451

452

453

454

455

456

457

458

459

460

461

462

463

464

465

466

467

468

469

470

471

472

473

474

475

476

477

478

479

480

481

482

483

484

485

486

487

488

489

490

491

492

493

494

495

496

497

498

499

500

501

502

503

504

505

506

507

508

509

510

511

512

513

514

515

516

517

518

519

520

521

522

523

524

525

526

527

528

529

530

531

532

533

534

535

536

537

538

539

540

541

542

543

544

545

546

547

548

549

550

551

552

553

554

555

556

557

558

559

560

561

562

563

564

565

566

567

568

569

570

571

572

573

574

575

576

577

578

579

580

581

582

583

584

585

586

587

588

589

590

591

592

593

594

595

596

597

598

599

600

601

602

603

604

605

606

607

608

609

610

611

612

613

614

615

616

617

618

619

620

621

622

623

624

625

626

627

628

629

630

631

632

633

634

635

636

637

638

5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042

[illegible]

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	52
--	---	---	---	---	---	---	---	---	---	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	----

200

360

360

QY 361 CTTACGGGATGCCCCACTCAGGTCACTTATGGAACCCCATGTCATTGGCATCAGCTTCAT 420
 Db 361 CTTACGGGATGCCCCACTCAGGTCACTTATGGAACCCCATGTCATTGGCATCAGCTTCAT 420
 QY 421 GGGCACTACATGATGGATGGGTGCCACACCCAGGCCATCGGGAGCCCAAGGCTTACT 480
 Db 421 GGGCACTACATGATGGATGGGTGCCACACCCAGGCCATCGGGAGCCCAAGGCTTACT 480
 QY 481 GGGCTGGGTGGTGGTGGTGGGAGCCCTGAGGTCCAACTATGTGCTCAAGAGACCGGGA 540
 Db 481 GGGCTGGGTGGTGGTGGTGGGAGCCCTGAGGTCCAACTATGTGCTCAAGAGACCGGGA 540
 QY 541 TGTGACGGTACACTCTCTCCAGGCAACAGCTTACCACTCTCCAGAAATTGGCCACA 600
 Db 541 TGTGACGGTACACTCTCTCCAGGCAACAGCTTACCACTCTCCAGAAATTGGCCACA 600
 QY 601 CTACGGCTCCCCCTGAGGCCCTGCTGATCCGACCCCATTCCTCCCTCCCATGGCCAAA 660
 Db 601 CTACGGCTCCCCCTGAGGCCCTGCTGATCCGACCCCATTCCTCCCTCCCATGGCCAAA 660
 QY 661 AACCCACTGTCTCTCTCCAAATTAAGATGTAGCTC 697
 Db 661 AACCCACTGTCTCTCTCCAAATTAAGATGTAGCTC 697

RESULT 3
 AF242517 724 bp mRNA linear PRI 15-AUG-2000
 LOCUS AF242517 Homo sapiens hypothetical protein SB168 mRNA, complete cds.
 DEFINITION AF242517.1 GI:9802032
 ACCESSION AF242517.1 GI:9802032
 VERSION AF242517.1 GI:9802032
 KEYWORDS

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 724)
 AUTHORS Man, T., Zhang, W. and Cao, X.
 TITLE Direct Submission
 JOURNAL Submitted (08-MAR-2000) Department of Immunology, Second Military Medical University & Shanghai Brilliance Biotechnology Institute, 800 Xiangyin Rd., Shanghai 200433, P.R. China

FEATURES
 source location/Qualifiers
 1..724
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 30..620
 /codon_start=1
 /product="hypothetical protein SB168"
 /protein_id="AA029598.1"
 /db_xref="GI:9802032"
 /translation="MSKRSMLIAMLPSLLRLHGAAGTETEDPACSPPIYPRYEWKALAS
 ECAOHSLPLRYVVSHTAGSSCNTPQQQARVVOHVMKTLGMCVGVNPLIGED
 GIVYGRGWNFLRYGASHGLAMPMISIGISTMGVMYDRVTPQAIRAAGILACGVAOGA
 LRSNYVLKSHRDVORTLSPGNOLYHLIQWPHYRSP"

ORIGIN

Query Match 99.7%; Score 695; DB 9; Length 724;
 Best Local Similarity 100.0%; Pred. No. 3.2e-143; Indels 0; Gaps 0;
 Matches 695; Conservative 0; Mismatches 0;

QY 3 CCGGACCTGCGGCGCTGACATATGCTCCGCGGCTCTATGCTGGCTGGGCTCTCC 62
 Db 3 CCGGACCTGCGGCGCTGACATATGCTCCGCGGCTCTATGCTGGCTGGGCTCTCC 62
 QY 7 CCGGACCTGCGGCGCTGACATATGCTCCGCGGCTCTATGCTGGCTGGGCTCTCC 66
 Db 7 CCGGACCTGCGGCGCTGACATATGCTCCGCGGCTCTATGCTGGCTGGGCTCTCC 66
 QY 63 CCGGACCTGCTGACTCGAGAGCGGCTCGAGAGACAGAAACCGGCGCTCTGACAGCCCA 122
 Db 63 CCGGACCTGCTGACTCGAGAGCGGCTCGAGAGACAGAAACCGGCGCTCTGACAGCCCA 122
 QY 67 CCGGACCTGCTTCCACTCGAGAGCGGCTCGAGAGACAGAAACCGGCGCTCTGACAGCCCA 126
 Db 67 CCGGACCTGCTTCCACTCGAGAGCGGCTCGAGAGACAGAAACCGGCGCTCTGACAGCCCA 126
 QY 123 TAGTGCCCGGGAAG 182
 Db 123 TAGTGCCCGGGAAG 182
 QY 127 TAGTGCCCGGGAAG 186
 Db 127 TAGTGCCCGGGAAG 186

QY 183 CCTACGCTATGTGTGTATGACACAGCGGGGAGAGCTGCAACACCCCGGCTGT 242
 Db 183 CCTACGCTATGTGTGTATGACACAGCGGGGAGAGCTGCAACACCCCGGCTGT 242
 QY 243 GCGAGACAGAGGCGCGGAATGTGACGACTACCTACATATGAACATATGGGCTGTGCGAG 302
 Db 243 GCGAGACAGAGGCGCGGAATGTGACGACTACCTACATATGAACATATGGGCTGTGCGAG 302
 QY 303 TGGGCTACAACTTCTGATTGAGAGAGAGGCTGTATACAGAGGCGGTGCTGAACT 362
 Db 303 TGGGCTACAACTTCTGATTGAGAGAGAGGCTGTATACAGAGGCGGTGCTGAACT 362
 QY 363 TCAAGGATGCCAATCAAGTCACTTATGGAACCCCATGCTCCATTGGCATCACTTCAG 422
 Db 363 TCAAGGATGCCAATCAAGTCACTTATGGAACCCCATGCTCCATTGGCATCACTTCAG 422
 QY 423 GCACTACATGGATGGGATGGGATGCCAAGCCAGGCCATCCGAGGAGGCTTATGG 482
 Db 423 GCACTACATGGATGGGATGGGATGCCAAGCCAGGCCATCCGAGGAGGCTTATGG 482
 QY 483 CTTGCGGTGTGGCTGACGAGAGCCCTGAGGTCCAACTATGTGCTCAAGAGACCGGAGT 542
 Db 483 CTTGCGGTGTGGCTGACGAGAGCCCTGAGGTCCAACTATGTGCTCAAGAGACCGGAGT 542
 QY 543 TGCAGGCTACACTCTCTCCAGGCAACAGCTTACCACTCTCCAGAAATTGGCCACT 602
 Db 543 TGCAGGCTACACTCTCTCCAGGCAACAGCTTACCACTCTCCAGAAATTGGCCACT 602
 QY 603 ACCGCTCCCGCTGAGGCGCTGCTGATCCGACCCCATTCCTCCCTCCCATGGCCAAA 662
 Db 603 ACCGCTCCCGCTGAGGCGCTGCTGATCCGACCCCATTCCTCCCTCCCATGGCCAAA 662
 QY 663 CCCCACTGTCTCTCTCCAAATTAAGATGTAGCTC 697
 Db 663 CCCCACTGTCTCTCTCCAAATTAAGATGTAGCTC 697

RESULT 4
 BD261706 726 bp DNA linear PAT 17-JUL-2003
 LOCUS BD261706 12 human secreted proteins.
 DEFINITION BD261706.1 GI:33071474
 ACCESSION BD261706.1 GI:33071474
 VERSION JP 2002530062-A/17.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 726)
 AUTHORS Ni, J., Ruben, S.M., Olsen, H.S., Young, P.E., Kenny, J.J., Moore, P.A., Wei, Y.F. and Greene, J.M.
 TITLE 12 human secreted proteins
 JOURNAL Patent: JP 2002530062-A/17 17-SEP-2002;
 HUMAN GENOME SCIENCES INC
 COMMENT OS Homo sapiens (human)
 PN JP 2002530062-A/17
 PD 17-SEP-2002
 PF 27-OCT-1999 JP 2000582421
 PI 28-OCT-1998 US 60/105971
 PT JIAN NI, STEVEN M RUBEN, HENRIK S OLSEN, PAUL E YOUNG, JOSEPH J KENNY,
 PI PAUL A MOORE, YING FEI WEI, JOHN M GREENE
 PC C12N15/09, A61K31/7088, A61K35/76, A61K38/00, A61K39/395, A61K39/
 PC 395, A61K48/00,
 PC A61P3/10, A61P7/00, A61P7/06, A61P9/10, A61P11/06, A61P17/02, A61P17/
 PC 06,
 PC A61P19/02, A61P25/16, A61P25/18, A61P25/22, A61P25/24, A61P25/28,
 PC A61P27/02,
 PC A61P27/06, A61P29/00, A61P29/00, A61P31/04, A61P31/18, A61P33/02,
 PC A61P33/04,
 PC A61P33/06, A61P35/00, A61P35/02, A61P37/02, A61P37/04, A61P37/06,
 PC

Db	452	GCAACTACATGGATGGGATGCCCAACCCCAAGCCATCCGGGCAAGCCCAAGGGGTCTACATCG	511
QY	483	CCTCGGATGNGSCTCAAGGAGCCCTGAGGTCCAACTATGTGTCTCAAGAGCAACCGGGATG	542
Db	512	CCTCGGGGTGGCTCAGGAGAGCCCTGAGGTCCAACTATGTGTCTCAAGAGCAACCGGGATG	571
QY	543	TGCAGCGTNACTCTCTCCAGGCAACCAAGCTCTACACCTCATCCAGATTGGCCCACT	602
Db	572	TGCAGCGTNACTCTCTCCAGGCAACCAAGCTCTACACCTCATCCAGATTGGCCCACT	631
QY	603	ACCGCTCCCCGTGAGGCCCTGTGTAATCCGACCCCAATTCCTCCCTCCCATGGCCAAAA	662
Db	632	ACCGTCCCCCGAAGCCCTGTGTAATCCGACCCCAATTCCTCCCTCCCATGGCCAAAA	691
QY	663	CCCCACTGTCTCTCTCCAAATAAAGATGTAGCTC	697
Db	692	CCCCACTGTCTCTCTCCAAATAAAGATGTAGCTC	726

RESULT 6					
AR226480					
LOCUS					
DEFINITION	AR226480	749 bp	DNA	linear	PAT 20-DEC-2002
ACCESSION	AR226480	Sequence 5 from patent US 6444790.			
VERSION	AR226480.1	GI:27265028			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 749)				
TITLE	Young, P.E., Ruben, S.M., Rosen, C.A. and Olsen, H.S.				
JOURNAL	Peptidoglycan recognition proteins				
FEATURES	Patent: US 6444790-A 5 03-SEP-2002;				
	Location/Qualifiers				
source	1..749				
	/organism="Unknown"				
	/mol_type="genomic DNA"				
ORIGIN					

Query Match	Similarity	99.7%	Score 695	DB 6	Length 749
Beet	Local	100.0%	Pred. No. 3.2e-143		
Matches	695	Conservative	0	Mismatches	0
			Indels		Gaps
			0		0
QY	3	CCGACCCCTGCGCCCTGCGCACTATGTCCCGCGCTATATGTGCTTGCTGGGCTCTCC	62		
Db	32	CCGGACCCCTGCGCCCTGCGCACTATGTCCCGCGCTATATGTGCTTGCTGGGCTCTCC	91		
QY	63	CCAGCTCTTTGACTTCGAGGGGGCTCAGAGACAGAAACCCGGCTGCTGCACGGCCA	122		
Db	92	CCAGCTCTTTGACTTCGAGGGGGCTCAGAGACAGAAACCCGGCTGCTGCAGGCCA	151		
QY	123	TATGCCCCGGAAACGAGTGAAGGCCCTGGGCATCAGAGTGGCGCCAGCACTGAGCTGC	182		
Db	152	TATGCCCCGGAAACGAGTGAAGGCCCTGGGCATCAGAGTGGCGCCAGCACTGAGCTGC	211		
QY	183	CCTTACGCTATGTGTGGTATTCGACACGGCGGGCGACGTGCAACATCCCCCGCTCGT	242		
Db	212	CCTTACGCTATGTGTGGTATTCGACACGGCGGGCGACGTGCAACATCCCCCGCTCGT	271		
QY	243	GCCAGACGAGCGGCCGGAATGTGCAGCACTACACATGAAGACACTGCGGTGGTGGACG	302		
Db	272	GCCAGACGAGCGGCCGGAATGTGCAGCACTACACATGAAGACACTGCGGTGGTGGACG	331		
QY	303	TGGGCTACAACTTCTGTATGAGAAACGGGCTCGTATTCGAGGGCCGTGTGAACT	362		
Db	332	TGGGCTACAACTTCTGTATGAGAAACGGGCTCGTATTCGAGGGCCGTGTGAACT	391		
QY	363	TCAAGGTGGCCACTCGAGTCACATTATGAAACCCCATGTGCATTGGGATCAGCTTATGG	422		
Db	392	TCAAGGTGGCCACTCGAGTCACATTATGAAACCCCATGTGCATTGGGATCAGCTTATGG	451		
QY	423	GCAACTACATGATCGGGTGGCCACACCCAGGCAATCGGGAGGCCACAGGTCTACTGG	482		

Db 452 GCAACTACATGGATGGGTGGCCACACCCAGAGCCATTCGGGGAGGCCACAGGGCTACTG 511

Qy 483 CTTGCGGGTGTGGCTCAGAGAGGCCCTGAGGTCCACTATGTGCTCAAAAGACACCGGGATG 542

Db 512 CTGCGGGTGTGGCTCAGAGAGGCCCTGAGGTCCACTATGTGCTCAAAAGACACCGGGATG 571

Qy 543 TGTAGGGTACACTCTCTCCAGGCAACAGCTCTACCACTATCCAGATTGGCCACT 602

Db 572 TGCAGGTACACTCTCTCCAGGCAACAGCTCTACCACTATCCAGATTGGCCACT 631

Qy 603 ACCGCTCCCCGTAGGCGCTGTCTATTCGGCACCCCATTCCTCCCTCCCATGGCCAAAA 662

Db 632 ACCGCTCCCCGTAGGCGCTGTCTATTCGGCACCCCATTCCTCCCTCCCATGGCCAAAA 691

Qy 663 CCCCACTGTCTCTTCTCCATTAAAGATGTAGCTC 697

Db 692 CCCCACTGTCTCTTCTCCATTAAAGATGTAGCTC 726

LOCUS	BD078857	718 bp	DNA	linear	PAT 27-AUG-2002				
DEFINITION	BD078857	Tumor proliferation inhibition- and apoptosis-associated gene and polypeptide and method of using the same.							
ACCESSION	BD078857								
VERSION	BD078857.1	GI:22624460							
KEYWORDS	JP 2001509384-A/2.								
SOURCE	Homo sapiens (human)								
ORGANISM	Homo sapiens								
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.								
AUTHORS	1 (baaes 1 to 718)								
TITLE	Georgiev,G., Kiselev,S., Prokhorchouk,E. and Ostermann,E.								
JOURNAL	Tumor proliferation inhibition- and apoptosis-associated gene and polypeptide and method of using the same								
COMMENT	Patent; JP 2001509384-A 2 24-JUL-2001; BOEHRINGER INGELHEIM INTERNATIONAL GMBH								
	OS Homo sapiens (human)								
	PN JP 2001509384-A/2								
	PD 24-JUL-2001								
	PF 10-JUL-1998 JP 2000502182								
	PR 11-JUL-1997 US 08/893764								
	PI GEORGI G,GEORGIEV, SERGEI KISELEV, EGOR PROKHORCHOUK, ELINBORG PI								
	OSTERMANN								
	PC C12N15/09,A61K35/76,A61K38/00,A61K48/00,A61P35/00,C07K4/525,								
	PC C07K16/24,								
	PC C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12P21/02,C12P21/08 PC								
	,C12Q1/68,G01N33/53,								
	PC C12N15/00,A61K37/02,C12N5/00								
	CC Tumor proliferation inhibition- and apoptosis-associated gene								
	CC and								
	CC polypeptide and method of using the same								
	PH Key								
	FT 5'UTR	Location/Qualifiers							
	FT CDS	1..67							
	FT 3'UTR	68..643							
	FT polyA site	644..718							
		712..714.							
		Location/Qualifiers							
FEATURES	1..718								
source	/organism="Homo sapiens"								
	/mol_type="genomic DNA"								
	/db_xref="taxon:9606"								

Query Match	96.7%	Score 674	D3 6	Length 718
Best Local Similarity	98.6%	Pred. No. 1.4e-138		
Matches 680	Conservative 0	Mismatches 10	Indels 0	Gaps 0

Qy	2	CCCGAGACCTGCGCGCCCTGCCACTATATGCCGCGCGCTATAGCTGCTCGGAGCTTTC	61
Db	29	CCCGAGACATATACCTCAGACCACTATATGCCGCGCGCTATAGCTGCTTTCCTCGGAGCTTTC	88

Db	89	CCGAGCCTCTTGGACTCCGAGCGCGCTCAGAGACAGAAACCCCGGCTGCTCAGGCC	148
QY	122	ATAGTCCCCGGAACGAGTGGAAAGCCCTTGCAATCAGAGTGGCCCCAGACCTTGACCTG	181
Db	149	ATAGTCCCCGGAACGAGTGGAAAGCCCTTGCAATCAGAGTGGCCCCAGACCTTGACCTG	208
QY	182	CCCTTACGATATGAGTGGTATGCGACACGCGCGGCGAGAGCTGCACACCCCGCTCG	241
Db	209	CCCTTACGATATGAGTGGTATGCGACACGCGCGGCGAGAGCTGCACACCCCGCTCG	268
QY	242	TGCCAGCAGCAGCGCCCGGAATGTGCAGACTTACCACTGAAAGACTGGGCTGTGTGGAC	301
Db	269	TGCCAGCAGCAGCGCCCGGAATGTGCAGACTTACCACTGAAAGACTGGGCTGTGTGGAC	328
QY	302	GTCGGCTACCACTTCTTGATTTGGAGAGAAGCGAGCTCGTATACGAGGCGCTGTGGAC	361
Db	329	GTCGGCTACCACTTCTTGATTTGGAGAGAAGCGAGCTCGTATACGAGGCGCTGTGGAC	388
QY	362	TTACGCGGTGCCACTCAGGTCACCTTATGGAACCCCATGTTCATTGGCATCAGTTTATG	421
Db	389	TTACGCGGTGCCACTCAGGTCACCTTATGGAACCCCATGTTCATTGGCATCAGTTTATG	448
QY	422	GGCAACTACATGGAATCGGGTCCCAACCCAGGCACTCCGAGCAGCCAGAGTCTACTG	481
Db	449	GGCAACTACATGGAATCGGGTCCCAACCCAGGCACTCCGAGCAGCCAGAGTCTACTG	508
QY	482	GCCTGCGGTGGCTCAGGAGACCTTGAGTTCACCTATGTGTCTTAAAGACACCGGGAT	541
Db	509	GCCTGCGGTGGCTCAGGAGACCTTGAGTTCACCTATGTGTCTTAAAGACACCGGGAT	568
QY	542	GTCGACGCTACACTCTTCCAGGCAACAGCTTACACACTCATCAGAAATTGGCCACAC	601
Db	569	GTCGACGCTACACTCTTCCAGGCAACAGCTTACACACTCATCAGAAATTGGCCACAC	628
QY	602	TACGCTCCCTTGAGGCTTGATTCGACCCCATTTCTCTCCCTCCATGGCCAAA	661
Db	629	TACGCTCCCTTGAGGCTTGATTCGACCCCATTTCTCTCCCTCCATGGCCAAA	688
QY	662	ACCCCACTGCTCCTTCCCAATAAAGATG	691
Db	689	ACCCCACTGCTCCTTCCCAATAAAGATG	718

RESULT 8	AF076483	690 bp	mRNA	linear	PI 15-AUG-1998
LOCUS	AF076483				
DEFINITION	Homo sapiens peptidoglycan recognition protein precursor (PGSP)				
ACCESSION	AF076483				
VERSION	AF076483.1	GI:3342532			
KEYWORDS	.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 690)				
TITLE	Kang,D., Liu,G., Lundstrom,A., Gelius,E. and Steiner,H.				
	A peptidoglycan recognition protein in innate immunity conserved from insects to humans				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 95 (17), 10078-10082 (1998)				
MEDLINE	98374308				
PubMed	9707603				
REFERENCE	2 (bases 1 to 690)				
AUTHORS	Kang,D., Liu,G., Lundstrom,A., Gelius,E. and Steiner,H.				
TITLE	Direct Submission				
JOURNAL	Submitted (08-JUL-1998) Microbiology, Stockholm University, Stockholm S-106 91, Sweden				
FEATURES	Location/Qualifiers				
source	1..690				

ORIGIN

Query Match	95.8%;	Score 667.8;	DB 9;	Length 690;
Best Local Similarity	99.7%;	Pred. No. 3.3e-137;		
Matches 669;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;

mat_peptide

sig_peptide

```

1. 690 /tissue_type="bone marrow"
/gene="PGRP"
45. 635 /gene="PGRP"
/codon_start="1"
/product="peptidoglycan recognition protein precursor"
/protein_id="PAC3182.1"
/db_xref="GI:334253"
/translacion="MSRRSWLLAWLPILRLRGAQETEDPACSPVIPRNEMALAS
EAGHLSIPRIYVVSHSTAGSSGPTASCOOARAVQHYHMTLLGMCVGVNPLIGET
GLVIEGKRMNTGASHSLINPISITISMGKMYRVPPIQAIRAAGQLACVAAGGA
LRSNVVLKGRDVRITSPENQILHLIQWPHYRS"
45. 104 /gene="PGRP"
/note="putative"
105. 632 /gene="PGRP"
/product="pepidoglycan recognition protein"

```

QY	301	CGTGGGCTACAACTTCTCTGATTTGGAGAAAGCGGCTCGTATACAGAGGCGGTGGTGGAA	360
Db	320	CGTGGGCTACAACTTCTCTGATTTGGAGAAAGCGGCTCGTATACAGAGGCGGTGGTGGAA	379
QY	361	CTTCAAGGGTGGCCACTCAGGTCACCTATATGAAGCCCATGTCCATTGGCATCAAGCTTCAT	420
Db	380	CTTCAAGGGTGGCCACTCAGGTCACCTATATGAAGCCCATGTCCATTGGCATCAAGCTTCAT	439
QY	421	GGGCAACTACATGATCGGATGCGCCACAACCCAGGCGATTCGGGCAAGCCCAAGGCTTCACT	480
Db	440	GGGCAACTACATGATCGGATGCGCCACAACCCAGGCGATTCGGGCAAGCCCAAGGCTTCACT	499
QY	481	GGCTTCGGGTGTGGCTCAGGAGAGCCCTGAGGTCGCAATATGTGTCAAAGAAACACGGGA	540
Db	500	GGCTTCGGGTGTGGCTCAGGAGAGCCCTGAGGTCGCAATATGTGTCAAAGAAACACGGGA	559
QY	541	TGAGCAGGCTACACTCTCTCCAGGAAACAACTCTACCACTCAATCCGAATTGGCCACA	600
Db	560	TGTGCAAGCTACACTCTCTCCAGGAAACAACTCTACCACTCAATCCGAATTGGCCACA	619
QY	601	CTACGGCTCCCTGAGGCGCTTGTGATCCGCAACCCATTCTCTCCCTCCCATAGGCCAAA	660
Db	620	CTACGGCTCCCTGAGGCGCTTGTGATCCGCAACCCATTCTCTCCCTCCCATAGGCCAAA	679
QY	661	AACTCCCACTGT 671	
Db	680	AACTCCCACTGT 690	

Mon May 17 11:03:26 2004

us-10-015-390a-215.rge

Page 7

RESULT 9
AX778312 537 bp DNA linear PAT 14-JUL-2003
LOCUS AX778312
SEQUENCE 469 from Patent WO03039443.
ACCESSION AX778312
VERSION AX778312.1 GI:32695306
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
Hafnerlach, T.; Schoch, C., Kern, W., Kohlmann, A., Schmitzger, S.,
Dugas, M., Ellis, R., Broers, B. and Wergenhaller, S.
Novel genetic markers for leukemias
Patent: WO 03039443-A 469 15-MAY-2003;
Deutsches Krebsforschungszentrum (DE);
Ludwig-Maximilians-Universitaet Muenchen (DE); Hafnerlach, Torsten,
PD Dr. Dr. (DE); Schoch, Claudia (DE); Kern, Wolfgang (DE)

FEATURES
source
Location/Qualifiers
1..537
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 77.0%; Score 537; DB 6; Length 537;
Best Local Similarity 100.0%; Pred. No. 2.6e-108;
Matches 537; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 CTTGACCTCGAGGCGCTCAGAGACAGAACCCCGGCTGCTCAGGCCCATAGTGC 130
DB 1 CTTGACCTCGAGGCGCTCAGAGACAGAACCCCGGCTGCTCAGGCCCATAGTGC 60
QY 131 CGGAACGAGTGAAGGCGCTCGCATCAGAGTGCAGCCCGCATCTGAGCTTCCCTTAC 190
DB 61 CGGAACGAGTGAAGGCGCTCGCATCAGAGTGCAGCCCGCATCTGAGCTTCCCTTAC 120
QY 191 TATGTGTGTGTATGCCACACGGCGGCGAGCGTGCACACCCCGCTGCTGCACAG 250
DB 121 TATGTGTGTGTATGCCACACGGCGGCGAGCGTGCACACCCCGCTGCTGCACAG 180
QY 251 CAGGCCCGGAATGTGCACACCTACCATGAGACACTGGGCTGTGTGCAGTGGGCTAC 310
DB 181 CAGGCCCGGAATGTGCACACCTACCATGAGACACTGGGCTGTGTGCAGTGGGCTAC 240
QY 311 AACTCTCTGATTGGAAGACCGGCTCTGTATACAGAGGCGCTGTGTGAACCTTCA 370
DB 241 AACTCTCTGATTGGAAGACCGGCTCTGTATACAGAGGCGCTGTGTGAACCTTCA 300
QY 371 GCCCACTAGCTCATTATGGAACCCCATGTCATTGCGATCAGCTTATGAGGCACTAC 430
DB 301 GCCCACTAGCTCATTATGGAACCCCATGTCATTGCGATCAGCTTATGAGGCACTAC 360
QY 431 ATGATCGGGTGCACACCCAGGCGCATCGGGGCAAGCCAGGCTTACTGGCTTGC 490
DB 361 ATGATCGGGTGCACACCCAGGCGCATCGGGGCAAGCCAGGCTTACTGGCTTGC 420
QY 491 GTGGCTCAGAGGCGCTGTGAGTCCAACTATGTGTCAAGAGCACCGGATGTGAGG 550
DB 421 GTGGCTCAGAGGCGCTGTGAGTCCAACTATGTGTCAAGAGCACCGGATGTGAGG 480
QY 551 AACACTCTTCACAGGCAACAGCTCTACCACTCATTCAGAAATGGCCCACTACCGC 607
DB 481 AACACTCTTCACAGGCAACAGCTCTACCACTCATTCAGAAATGGCCCACTACCGC 537

RESULT 10
CDR3J1676 700 bp mRNA linear MAM 21-DEC-2000
LOCUS CDR3J1676
DEFINITION Camelus dromedarius mRNA for peptidoglycan recognition protein.
ACCESSION AJ131676

VERSION AJ131676.1 GI:11990123
KEYWORDS
peptidoglycan recognition protein.
SOURCE
ORGANISM
Camelus dromedarius (Arabian camel)
Eukaryota; Metazoa;
Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
REFERENCE
AUTHORS
TITLE
Kappeler, S.R., Farah, Z. and Puhari, Z.
Milk as a Source of Camel (Camelus dromedarius) Peptidoglycan
Recognition Protein
Unpublished
2 (bases 1 to 700)
REFERENCE
AUTHORS
TITLE
Kappeler, S.R.
Direct Submission
Submitted (21-DEC-1998) Kappeler S.R., Institute of Food Science,
Swiss Federal Institute of Technology, LFO F26, 8092 Zurich,
SWITZERLAND

FEATURES
source
Location/Qualifiers
1..700
/organism="Camelus dromedarius"
/mol_type="mRNA"
/sub_species="Somali breed"
/db_xref="taxon:9838"
/tissue_type="lactating mammary gland"
25..606
/codon_start=1
/product="peptidoglycan recognition protein"
/protein_id="CAC19553.1"
/db_xref="GI:11990124"
/db_xref="GDB:O96K12"
/db_xref="SPTREMBL:O96K12"
/translation="MTKICVLVWMLALSLGAREPPACGSIVPRRPPALASEC
RELTRPVYVSHSHCHDTPASCAQQAQNVSYVRNDGWDVFNPLIGDGL
VYEGRGMMKGAHAGPTWNPDISIGISFMGNVNRVPPRALRAQNLACGVLAGLR
SNVEYKGRHDVPTLSPDRIVEIETMSHYRA"

CDS

sig_peptide
mat_peptide
polyA_signal
ORIGIN

Query Match 56.5%; Score 394; DB 4; Length 700;
Best Local Similarity 77.0%; Pred. No. 9.8e-77;
Matches 522; Conservative 0; Mismatches 145; Indels 11; Gaps 3;

QY 24 CTATGTCCCGCGCTATAGCTGCTGCTGAGGCTTCCAGCTCTTCACTGGAG 83
DB 23 CATGACCCGCGCACTCGTCTTCTGCTGAGGCTTCCGCTTCCAGGCTCGAG 82
QY 84 CGGCTCAGAGAGAGAGAACCCGCGCTGCGACAGCCCATAGAGCCCGGAAGTGA 143
DB 83 CGGCTC-----AGAGACCCGCGCTGCGCTGCGCTCATCGTCCCGGAGATGA 136
QY 144 AGGCGCTGCGATGAGTGCAGCCAGACCTGAGCTGCTTACGCTATGTGTGTAT 203
DB 137 GGGGCTGCGGTCCAGGTGAGAGAAAGGTACAAGGCGGCTGCTGCTGCTGCTG 196
QY 204 CGCACAGGCGGCGAGAGTGTCAACACCCCGCTCTGCGCAGAGAGCGCCGGAATG 263
DB 197 CGCACAGGCGGCGAGAGTGTCAACACCCCGCTCTGCGCAGAGAGCGCCGGAATG 256
QY 264 TGCAGCACTACCAATGAAGACACTGGGCTGTGTGCAAGTGGCTCAACTTCTGATTG 323
DB 257 TGCAGCACTACCAATGAAGACACTGGGCTGTGTGCAAGTGGCTCAACTTCTGATTG 316
QY 324 GAGAGAGCGGCTGTATACAGAGGCGCTGTGTGCAAGTGGCTCAACTTCTGATTG 383
DB 317 GAGAGAGTGGGCTGTGTATGAGAGCGCGAGGCTGTGAACATCAAGGCGCCAGAGATC 376
QY 384 ACTATGAGAACCCCATGCTTGCATTCAGCTTCACTGAGGCACTACATGATGAGTGC 443
DB 377 CCAGCTGAAACCCCATGCTTGCATTCAGCTTCACTGAGGCACTACATGATGAGTGC 436

QY 444 CCACACCCAGCCATCCGAGGAGCCAGGAGCTTACTGAGCTGCGGTGTGCTCAGGAG 503
 DB 437 CCCCCCCCCCGGCCCCCTCCGGGCAAGCAATCTGTGGCTTGTGTGTGGCTCTCGGAG 496
 QY 504 CCTTGAAGTCCATCTATGTGTCAAGAAGCAACCGGATGTGACAGCTACTCTCTCAG 563
 DB 497 CCTTGAAGTCCATCTATGTGTCAAGAAGCAACCGGATGTGACAGCTACTCTCTCAG 556
 QY 564 GCAACACGCTCTACCACTTCATCCAGAAATGGCCACACTACCGCTCCCTGAGGAGCCCTG 623
 DB 557 GTGACCGGCTCTACAGAAATTCATCCAGAAATGGCCACACTACCGCTCCCTGAGGAGCCCTG 615
 QY 624 CTGATCCGACCCCACTTCTCTCCCTCCATGAGCCCAAAACCCCACTG---TCTCTTCT 679
 DB 616 CCGCTGCGACACCGCTCCCATCCCTGCTGTCTGTCAAAACCCCACTGCTCTCTCCCTCC 675
 QY 680 CCAATAAGATGTAGCTC 697
 DB 676 CCAATAAGATGTAGCTC 693

RESULT 11
 BD204097 380 bp DNA linear PAT 17-JUL-2003
 LOCUS 5'EST and human protein encoded thereby.
 ACCESSION BD204097.1 GI:33013867
 VERSION BD204097.1
 KEYWORDS JP 2002511259-A/301.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 380)
 AUTHORS Edwards,J.B.D.M., Duclert,A. and Giordano,J.Y.
 TITLE 5'EST and human protein encoded thereby
 JOURNAL Patent: JP 2002511259-A 301 16-APR-2002;
 GENESET

COMMENT OS Homo sapiens (human)
 PN JP 2002511259-A/301
 PD 16-APR-2002
 PR 09-APR-1998 JP 2000543599
 PR 09-APR-1998 US 09/057719,28-APR-1998 US 09/069047 PI
 JEAN BAPTISTE DUMAS MILNE EDWARDS, AYMERIC DUCLERT, JEAN YVES PI
 GIORDANO
 PC C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12M1/00, C12N1/15, PC
 C12N1/19,
 PC C12N1/21, C12N5/10, C12P21/02, C12Q1/68, G01N33/53, G01N33/566, PC
 G06F17/50//
 PC G06F17/30, C12N15/00, C12N5/00, C12N15/00
 CC Von Heljne matrix
 CC score 5.6999980926514
 CC seq LAMWALPSLRIGA/AQ
 CC n=a, g, c or t
 FH Key Location/Qualifiers
 FT CDS 33..380
 FT sig_peptide 33..92
 FT sig_feature 326.
 FT misc_feature Location/Qualifiers
 1..380
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

ORIGIN

Query Match 51.3%; Score 357.4; DB 6; Length 380;
 Best local similarity 98.1%; Pred. No. 1.3e-68;
 Matches 366; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

QY 1 TCCCGAGCCCTGCGGCGCTGCACTATGTCGCGGCGCTCTATGCTGCTGCGGCTCT 60
 DB 8 TCCCGAGCCCTGCGGCGCTGCACTATGTCGCGGCGCTCTATGCTGCTGCGGCTCT 67
 QY 61 CCCAGGCTCTCTGACTCGAGGCGCTCAGAGAGACAGAAAGACCCGCGCTCTGCAAGCC 120

DB 68 CCCCCGCTCTTCGACTCTGAGCGGCTCTGAGAGCAAGAACCCGGCTGTGTGAGCCC 127
 QY 121 CATAGTCCCGGAACGATGGAAGCCCTGCGCATGAGTGCCTCCAGCACTTGAAGCT 180
 DB 128 CATAGTCCCGGAACGATGGAAGCCCTGCGCATGAGTGCCTCCAGCACTTGAAGCT 187
 QY 181 GCGCTTACGCTATGTGTGTGTATCGACACGCGGCGGAGCAGCTGGAACACCCCGGCTC 240
 DB 188 GCGCTTACGCTATGTGTGTGTATCGACACGCGGCGGAGCAGCTGGAACACCCCGGCTC 247
 QY 241 GTGCGACGACAGGCGCGGAATGTGACGACCTACCAATGAAGACACTGGCTGTGCGA 300
 DB 248 GTGCGACGACAGGCGCGGAATGTGACGACCTACCAATGAAGACACTGGCTGTGCGA 307
 QY 301 CGTGGCTACACTTCTT-GATTGAGAGAGCGGCTGTATACGAGGCGGCTGTGCGA 359
 DB 308 CGTGGCTACACTTCTTGTGATTTGAGAGAGCGGCTGTATACGAGGCGGCTGTGCGA 367
 QY 360 ACTTCAAGGCTGC 372
 DB 368 ACTTCAAGGCTGC 380

RESULT 12
 AY083309 688 bp mRNA linear NAM 29-MAY-2002
 LOCUS Bos taurus oligosaccharide-binding protein mRNA, complete cds.
 DEFINITION AY083309
 ACCESSION AY083309
 VERSION AY083309.1 GI:19550241
 KEYWORDS Bos taurus (cow)
 SOURCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bos.
 ORGANISM Bos taurus

REFERENCE 1 (bases 1 to 688)
 AUTHORS Tydeli,C.C., Yount,N., Tran,D., Yuan,J. and Seleted,M.B.
 TITLE Isolation, characterization, and antimicrobial properties of bovine oligosaccharide-binding protein. A microbicidal granule protein of eosinophils and neutrophils
 JOURNAL J. Biol. Chem. 277 (22), 19658-19664 (2002)
 PUBMED 11860375
 MISCNAME 2 (bases 1 to 688)
 Yount,N.Y., Yuan,J., Tydeli,C.C. and Seleted,M.B.
 REFERENCE Direct Submission
 AUTHORS Submitted (11-MAR-2002) Pathology, UC Irvine, 440D Medical Sciences
 JOURNAL 1, Irvine, CA 92697, USA
 FEATURES
 source Location/Qualifiers
 1..688
 /organism="Bos taurus"
 /mol_type="mRNA"
 /db_xref="taxon:9913"
 /cell_type="peripheral white blood cells"
 29..601
 /note="microbicidal; undergoes N-terminal glutamine cyclization; peptidoglycan recognition protein; PGRP"

CDS

misc_feature
 order(98..100,470..472)
 /note="disulfide bond"
 misc_feature
 order(146..148,281..283)
 /note="disulfide bond"
 misc_feature
 order(209..211,227..229)
 /note="disulfide bond"

ORIGIN

AUTHORS	TITLE	TOTMNT
SLAYTON, W.B., RIGAAI, A., HANCOCK, J.D., ZANG, J.K., LE, T.V., TRAUTMAN, M.S., SPANGRUDE, G.J., CARROLL, W.L. and SCHIBLER, K.R.	Direct Submission	Submitted (11 Oct 1990)